

### C. Remarks

The claims are 28-33, with claims 28, 30, 32, and 33 being independent. The independent claims have been amended to better define the invention. Support for the amendment may be found throughout the specification, for example, in the First to Third Embodiments, as well as in Figs. 1-3. No new matter has been added. Reconsideration of the present claims is expressly requested.

Claims 32 and 33 stand rejected under 35 U.S.C. § 101 as being allegedly directed to non-statutory subject matter. Specifically, the Examiner alleged that these claims do not comply with the requirements set forth in the *In re Bilski* case, because the recited steps are not tied to a particular machine (because all of the steps can allegedly be performed mentally) and they do not require any particular article to be transformed into another state or thing.

Claims 32 and 33 have been amended to clarify that test information is generated and outputted to a computer readable storage medium. Thus, Applicant respectfully submits that claims 32 and 33 satisfy the requirements of 35 U.S.C. § 101, as articulated by the Federal Circuit in the *In re Bilski* case. Thus, withdrawal of the above rejection is respectfully requested.

Claims 28-33 stand rejected under 35 U.S.C. § 103(a) as being allegedly obvious from U.S. Patent Application Publication No. 2002/0110823 A1 (Hogan); 2005/0064436 A1 (Barrett); or 2004/0048259 A1 (Hashmi) in view of U.S. Patent Nos. 6,238,869 B1 (Kris) and 5,876,926 (Beecham). The grounds of rejection are respectfully traversed.

Claims 28 and 30 recite a testing method, which utilizes a DNA microarray. In this method, the DNA microarray is hybridized with a solution of DNA including genes suitable for personal identification and disease-related genes extracted from a specimen of a particular subject. The DNA microarray includes a first DNA probe group, which reacts with the genes suitable for personal identification and is capable of being used to identify a subject, and a second DNA probe group, which reacts with the disease-related genes. Also, the DNA microarray has two separated areas, one of which is an area where probes of the first DNA probe group are arranged and the other is an area where probes of the second DNA probe group are arranged. Due to carrying out the test using a microarray with such an arrangement, identification can be easily performed from a hybridization pattern. In addition, this method makes it easy to change a probe design for disease-related genes.

The Examiner has acknowledged that neither Hogan, Barrett, nor Hashmi teaches a DNA microarray with two separate areas as claimed. However, the Examiner has cited Kris for this disclosure. Applicant respectfully disagrees.

Kris is directed to a high throughput assay system. This reference teaches a DNA microarray with a plurality of areas. According to Kris, to perform multiple, high throughput, biological or chemical assays, a plurality of substantially identical, spatially discrete (separated) regions are arranged on a DNA array as shown in Fig. 1 (Abstract; col. 3, lines 33-36). As a result Kris can perform the same tests with regard to multiple kinds of DNA solutions at the same time.

However, like the other cited references, Kris fails to disclose or suggest a DNA microarray including areas with different probe groups. That is, Kris fails to teach or

suggest a DNA microarray having an area with a first DNA probe group, which reacts with the genes suitable for personal identification and is capable of being used to identify a subject, and an area with a second DNA probe group, which reacts with the disease-related genes and is capable of being used to check the health condition of a subject. According to the present invention, two types of genes (a gene suitable for personal identification of the subject and a gene suitable for checking health condition of the subject) can be detected at the same time.

As recited in claims 32 and 33, a testing method in accordance with the present invention may also include comparing identification information acquired from the hybridization result of the first DNA probe group with identification information stored in a storage device and analyzing the hybridization state of the second DNA probe group if the comparison indicates that both sets of identification information match. Thus, when identification is successful, there is a high probability that hybridization is successful, and the state of the disease of a subject can be determined quickly and accurately.

The Examiner alleged that the “comprising” language in claims 32 and 33 does not limit the claims to a method in which the hybridization state of the second DNA probe group is analyzed only when the information is determined to match. While Applicant disagrees with the Examiner’s interpretation of these claims, claims 32 and 33 have now been amended to explicitly state that the analysis is performed only when the identification information matches.

The Examiner alleged that Beecham's method reads on claims 32 and 33, because no test information is released when the biometric data does not match the stored biometric data (column 18, lines 14-19). Applicant respectfully disagrees.

The Examiner has interpreted the biometric data submitted by the user in Beecham as the identification information from the microarray and the stored biometric data as the identification information on the medical card. Applicant submits, however, that the transmittal of records referred to by Beecham, which occurs when a biometric data match is found, is different from the generation and analysis related to the second DNA probe group recited in claims 32 and 33.

In conclusion, Applicant respectfully submits that the cited references, whether considered separately or in any combination, fail to disclose or suggest the presently claimed elements.

Wherefore, expedient allowance of the claims and passage to issue are respectfully requested.

Applicant's undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

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